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TTGAAATTATCTGGTCACTGCCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGTCTGA  
GGCGGGTGGACCACCTGGGGTCAGGAGTTTCGAGACCAGGCTGGCCAACATGGCGAAACCTGACTACA  
CAAAAAACACAAAATTTAGCCGGGGCTTGGGCGCTCCTGTGCTCCCAGCTACTCAGGAGGCTGAGGTG  
GGAGGACTGCTTGAGCCTGGGAGGTGAGGCTGCAGTGAGCTGTGATCGCGCCACTTAACTCCAGCC  
TGGACGACAGTGAGACCCTGTCTCAAGAAGAAAAAAGAAAGAAAGAAAAAAGAAAAAAGAAAAAAGAA  
AATTATTTGGTCAATTATATGGTCAGTCCCTCCACCACTCGCGAATTTACAGAAGAGGAGAAGTGGG  
CTGGGCGAGACCAGGACTAGCCCAAGATTACACAAGTTACTCGGTTGTAGAGCCAGGATTAGACAGGA  
GAGGCTCTAGATTCTGGTCTAGACTCCCCTCCTATTATTTAGCATTATGGCTTCCTGAGGATTACCAT  
GAGCCCTCCTCCACCGTCAAGCGGCAGCTACCAGCCACCAGACCAGATCCCTTCGAAGGTGCCCGGAG  
TACCAGACTGACAAAAGCGCCCGTACAGTGCTCAGTCTGTAAACCAAAGCTGTCTAGGGTGCAGACAT  
CGCTCACCGGACCGGGTAGGGCTCGTGCGCTAAGGGCGCCGGGTATTCCAGTTAGTGGAGAGGGAAGC  
GCCCTGGAAGTGCATGGGCCCCGGGAGAGGGCGCGGGAGCGGAGCATGGCCGGGCGGGGCGGGCCGCG  
GCCGTGGGCGGAGACTGCGCGCAGCTAGCTCGGGAGCGCCTCGGAGCC QCCCCGAGAGCCGCTTCT  
CGCGCCCCGAGCGCAGCGCAGCGCTCCGCCGTCTGACCTGCCGCGCCCGCAGCGTGCGGGCTGGGAA  
AGGAGGCGCTCACCGAGAGGGACACGCGCCAGGCTCCAGCCCGACCCGGGACGCGGCGGGCCGCGCG  
GAGCACCCATGGGCAGCCCTGGAACGGCAGCGACGGCCCCGAGGGGGCGCGGGAGCCGCCGTGGCCC  
GCGCTGCCGCCTTGCGACGAGCGCCGCTGCTCGCCCTTTCCCCTGGGGGCGCTGGTGCCGGTGACCGC  
TGTGTGCCTGTGCCTGTTTCGTCTCGGGGTGAGCGGCAACGTGGTGACCGTGATGCTGATCGGGCGCT  
ACCGGGACATGCGGACCACCACCAACTTGTACCTGGGCAGCATGGCCGTGTCCGACCTACTCATCTG  
CTCGGGCTGCCGTTTCGACCTGTACCGCTCTGGCGCTCGCGGCCCTGGGTGTTCCGGGCCGCTGCTCTG  
CCGCCTGTCCCTCTACGTGGGCGAGGGCTGCACCTACGCCACGCTGCTGCACATGACCGCGCTCAGCG  
TCGAGCGCTACCTGGCCATCTGCCGCCCGCTCCGCGCCCGCGTCTTGGTCACCCGGGCGCCGCTCCGC  
GCGCTCATCGCTGTGCTCTGGGCCGTGGCGCTGCTCTCTGCCGGTCCCTTCTTGTTCTTGGTGGGCGT  
CGAGCAGGACCCCGGCATCTCCGTAGTCCCGGGCTCAATGGCACCGCGCGGATCGCTCCTCGCCTC  
TCGCCTCGTCGCCGCTCTCTGGCTCTCGCGGGCGCCACCGCCGTCCCCGCCGTGGGGCCCCGAGACC  
GCGGAGGCCGCGGCGCTGTTTCAGCCGCGAATGCCGGCCGAGCCCCGCGCAGCTGGGCGCGCTGCGTGT  
CATGCTGTGGGTACCAACCGCCTACTTCTTCTGCCCTTTCTGTGCCTCAGCATCCTCTACGGGCTCA  
TCGGGCGGGAGCTGTGGAGCAGCCGGCGGCCGCTGCGAGGCCCGGCCGCTCGGGGCGGGAGAGAGGC  
CACCGGCAGACCGTCCGCGTCTGCgtaagtggagccgctggttccaaagacgcctgcctgcagtc  
cgccccgcgggggaccgcgcaaagcctccctcccttcccttgcctgcgccagctctggtgcgcgcttc  
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cctgtccccccaggagctctgggggaccccagggcgctttgaggggtgggatccccggatccgattcagt  
aaccagcagtgcttttccagagcctctgagaccagaaaggagagttggtattcttaattccaaccacc  
tgtagatgccacaaatgaggagtcctcacagtgctcttgagaagacgagggagatttcattaagcta  
aaatTTTTtatttaattgtaagtgtgtaaggctaaagtaaacttgctcgatatcaaaaagtaaag  
attgtgcagacctgtttagaattcttttcaacagagaacagaaaacttgcttccgaagtgggtttgt  
ggaaggaagcctgccaaaggcgcttggtcagagaaattgctccttctggtttatgtccagccttgata  
acacatatgggagcctactatgcagttttaagcaagtatccatgcagcctgcagcctgggtcattttt  
tctgggggtgaggatctgcctaggtagaagttttctctaattttattttgctgttacttggtattgcaga  
tggttccttgctcggggtggggggtttatttgcttccaatgcttttggttaatcccgggtgctgtgtctt  
atgttgtagTGGTGGTGGTCTGGCATTATAATTTGCTGGTTGCCCTTCCACGTTGGCAGAATCATT  
TACATAAACACGGAAGATTGCGGATGATGTACTTCTCTCAGTACTTTAACATCGTCGCTCTGCAACT  
TTTCTATCTGAGCGCATCTATCAACCAATCCTCTACAACCTCATTTCAAAGAAGTACAGAGCGGCGG  
CCTTTAACTGCTGCTCGCAAGGAAGTCCAGGCCGAGAGGCTTCCACAGAAGCAGGGACACTGCGGGG  
GAAGTTGCAGGGGACACTGGAGGAGACACGGTGGGCTACACCGAGACAAGCGCTAACGTGAAGACGAT  
GGGATAA

FIG. 1

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ATGGGCAGCCCTGGAACGGCAGCGACGGCCCCGAGGGGGCGCGGGAGCCGCGTGGCCCCGCGCTG  
CCGCCTTGCGACGAGCGCGCTGCTCGCCCTTTCCCCTGGGGGCGCTGGTGCCGGTGACCGCTGTG  
TGCTGTGCCTGTTCTGTCGTCGGGGTGAGCGGCAACGTGGTGACCGTGATGCTGATCGGGCGCTAC  
CGGGACATGCGGACCACCACCAACTTGTACCTGGGCAGCATGGCCGTGTCCGACCTACTCATCTG  
CTCGGGCTGCCGTTTCGACCTGTACCGCCTCTGGCGCTCGCGGCCCTGGGTGTTGGGGCCGCTGCTC  
TGCCGCCTGTCCCTCTACGTGGGCGAGGGCTGCACCTACGCCACGCTGCTGCACATGACCGCGCTC  
AGCGTCGAGCGCTACCTGGCCATCTGCCGCCCGCTCCGCGCCCGCGTCTTGGTCACCCGGCGCCGC  
GTCCGCGCGCTCATCGCTGTGCTCTGGGCCGTGGCGCTGCTCTCTGCCGTCCTTCTTGTTCCCTG  
GTGGGCGTCGAGCAGGACCCCGGCATCTCCGTAGTCCCGGGCCTCAATGGCACC GCGCGGATCGCC  
TCCTCGCCTCTCGCCTCGTCGCCGCTCTCTGGCTCTCGCGGGCGCCACCGCCGTCCCCGCCGTCG  
GGGCCCCGAGACCGCGGAGGCCGCGGCGCTGTTCAAGCGGAATGCCGGCCGAGCCCCGCGCAGCTG  
GGCGCGCTGCGTGTCATGCTGTGGGTCAACACCGCCTACTTCTTCTGCCCTTTCTGTGCCTCAGC  
ATCCTCTACGGGCTCATCGGGCGGGAGCTGTGGAGCAGCCGGCGGCCGCTGCGAGGCCCGGCCGCC  
TCGGGGCGGGAGAGAGGCCACCGGCAGACCGTCCGCGTCCTGCTGGTGGTGGTTCTGGCATTATA  
ATTTGCTGGTTGCCCTTCCACGTTGGCAGAATCATTTACATAAACACGGAAGATTCGCGGATGATG  
TACTTCTCTCAGTACTTTAACATCGTCGCTCTGCACTTTTCTATCTGAGCGCATCTATCAACCCA  
ATCCTCTACAACCTCATTTCAAAGAAGTACAGAGCGGCGGCCTTAACTGCTGCTCGCAAGGAAG  
TCCAGGCCGAGAGGCTTCCACAGAAGCAGGGACACTGCGGGGGAAGTTGCAGGGGACACTGGAGGA  
GACACGGTGGGCTACACCGAGACAAGCGCTAACGTGAAGACGATGGGATAA

FIG.2

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MGSPWNGSDGPEGAREPPWPALPPCDERRCSPFPLGALVPVTAVCLCLFVVGVSNGNVVTVMLIGRY  
RDMRTTTNLYLGSMVSDLLILLGLPFDLYRLWRSRPWFPGPLLCRLSLYVGEGETYATLLHMTAL  
SVERYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFLFLVGVEQDPGISVVPGLNGTARIA  
SSPLASSPPLWLSRAPPPSPPSGPETAEEAALFSRECRPSPAQLGALRVMLWVTTAYFFLPFLCLS  
ILYGLIGRELWSSRRPLRGPAASGRERGRHRTVRVLLVVVLAFIICWLPFHVGRIIYINTEDSRMM  
YFSQYFNIVALQLFYLSASINPILYNLISKXYRAAAFKLLARKSRPRGFHRSRDTAGEVAGDTGG  
DTVGYTETSANVKTMG

FIG.3

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ATGGGCAGCCCCTGGAACGGCAGCGACGGCCCCGAGGGGGCGCGGGAGCCGCGTGGCCCCGCGCTG  
CCGCCTTGCGACGAGCGCCGCTGCTCGCCCTTTCCCTGGG&GCGCTGGTGCCGGTGACCGCTGTG  
TGCCTGTGCCTGTTTCGTCGTCGGGGTGAGCGGCAACGTGGTGACCGTGATGCTGATCGGGCGCTAC  
CGGGACATGCGGACCACCACCAACTTGTACCTGGGCAGCATGGCCGTGTCCGACCTACTCATCCTG  
CTCGGGCTGCCGTTTCGACCTGTACCGCCTCTGGCGCTCGCGGCCCTGGGTGTTCCGGGCCGCTGCTC  
TGCCGCCTGTCCCTCTACGTGGGCGAGGGCTGCACCTACGCCACGCTGCTGCACATGACCGCGCTC  
AGCGTCGAGCGCTACCTGGCCATCTGCCGCCCCGCTCCGCGCCCGCTCTTGGTCACCCGGCGCCGC  
GTCCGCGCGCTCATCGCTGTGCTCTGGGCCGTGGCGCTGCTCTCTGCCGGTCCCTTCTTGTTCCCTG  
GTGGGCGTCGAGCAGGACCCCGGCATCTCCGTAGTCCCGGGCCTCAATGGCACC GCGCGGATCGCC  
TCCTCGCCTCTCGCCTCGTCGCCGCTCTCTGGCTCTCGCGGGCGCCACCGCCGTCCCCGCCGTGCG  
GGGCCCCGAGACCGCGGAGGCCGCGGCGCTGTTAGCCGCGAATGCCGGCCGAGCCCCGCGCAGCTG  
GGCGCGCTGCGTGTCATGCTGTGGGTACCAACCGCCTACTTCTTCTGCCCTTTCTGTGCCTCAGC  
ATCCTCTACGGGCTCATCGGGCGGGAGCTGTGGAGCAGCCGGCGGCCGCTGCGAGGCCCGGCCGCC  
TCGGGGCGGGAGAGAGAGGCCACCGGCAGACCGTCCGCGTCTGCGTAAGTGGAGCCGCCGTGGTTCC  
AAAGACGCCTGCCTGCAGTCCGCCCCGCCGGGACCGCGCAAACGCTGGGTCCCTTCCCCTGCTC  
GCCCAGCTCTGGGCGCCGCTTCCAGCTCCCTTTCTATTTGATTCCAGCCTCCACCCGCCGTGGT  
GGTGGTTCTGGCATTATAATTTGCTGGTTGCCCTTCCAGTTGGCAGAATCATTTACATAAACAC  
GGAAGATTGCGGATGATGTACTTCTCTCAGTACTTTAACATCGTCGCTCTGCAACTTTTCTATCT  
GAGCGCATCTATCAACCAATCCTCTACAACCTCATTTCAAAGAAGTACAGAGCGGCGGCCTTTAA  
ACTGCTGCTCGCAAGGAAGTCCAGGCCGAGAGGCTTCCACAGAAGCAGGGACACTGCGGGGGAAGT  
TGCAGGGGACACTGGAGGAGACACGGTGGGCTACACCGAGACAAGCGCTAACGTGAAGACGATGGG  
ATAA

FIG.4

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MGSPWNGSDGPEGAREPPWPALPPCDERRCSPFPLGALVPVTAVCLCLFVVGVSNGNVVIVMLIGRY  
RDMRTTTNLYLGSMVSDLLILLGLPFDLYRLWRSRPWVFGPLLCLSLYVGEGCTYATLLHMTAL  
SVERYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFLFLVGVEQDPGISVVPGLNGTARIA  
SSPLASSPPLWLSRAPPPSPPSGPETAEEAALFSRECRPSPAQLGALRVMLWTTAYFFLPFLCLS  
ILYGLIGRELWSSRRPLRGPAASGREGRGHRQTVRVLRKWSRRGSKDACLOSAPPGTAQTLGPLPLL  
AQLWAPLPAPFPISIPASTRRGGGSGIYNLLVALPRWQNHLLHKHGRFADDVLLSVL

FIG.5

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1 M G S P W N G AAC GGC AGC GAC GGC CCC GAG GGG GCG CCG GAG CCG CCG TGG CCC GCG CTG CCG CCT TGC  
 GAC GAG CGC CGC TGC TCG CCC TTT CCC CTG GGG <sup>TM1</sup>CTG GCG CTG GTG CCG GTG ACC GCT GTG TGC CTG TGC CTG TTC GTG  
 D E R C S P F P L G A L V P V T A V C L C L F V  
 GTC GGG GTG AGC GGC AAC GTG GTG ACC GTG ATG CTG ATC GGG CCG TAC CCG GAC ATG CCG ACC ACC ACC AAC TTG  
 V G V S G N V V T V M L I G R Y R D M R T T T T N L  
 TAC CTG GGC AGC <sup>TM2</sup>ATG GGC TCC GAC CTA CTC ATC CTG CTC GGG CTG GAC TTC GAC CTG TAC CCG CTC TGG CGC  
 Y L G S M A V S D L L I L L G L G L F D L Y R L W R  
 TCG CGG CCC TGG GTG TTC GGG CCG CTG CTC TGC CGC <sup>TM3</sup>CTG TCC CTC TAC GTG GGC GAG GGC TGC ACC TAC GCC ACG  
 S R P P W V F G P L L C R L S L Y V G E G C T Y A T  
 CTG CTG CAC ATG ACC GCG CTC AGC GTC GAG CGC TAC CTG GCC ATC TGC CGC CCG CTC CGC GGC CTC TTG GTG  
 L L H M T A L S V E R Y L A I C R P L R A R V L V  
 ACC CGG CGC CGC GTC CGC CTC <sup>TM4</sup>ATC GCT GTG CTC TGG GCC GTG GCG CTG CTC TCT GGC GGT CCC TTC TTG TTC  
 T R R R V R A L I A V L W A V A L L S A G P F L F  
 CTG GTG GGC GTC GAG CAG GAC CCC GGC ATC TCC GTA GTC CCG GGC CTC AAT GGC ACC GCG CCG ATC GCC TCC TCG  
 L V G V E Q D P G I S V V P G L N G T A R I A S S  
 CCT CTC GCC TCG CCG CCT CTC TGG CTG TCG CGG GCG CCA CCG CCG TCC CCG CCG TCG GGG CCC GAG ACC GCG  
 P L A S S P P L W L S R A P P P S P P S G P E T A  
 GAG GCC GCG GCG CTG TTC AGC CGC GAA TGC CGG CCG AGC CCC GCG CAG CTG GGC CCG CTG CGT <sup>TM5</sup>GTC ATG CTG TGG  
 E A A A L F S R E C R P S P A Q L G A L R V M L W  
 GTC ACC ACC GCC TAC TTC CTG CCC TTT CTG TGC CTC AGC ATC CTC TAC GGG CTC ATC GGG CGG GAG CTG TGG  
 V T T A Y F L P L C L S I L Y G L I G R E L W  
 AGC AGC CGG CGG CCG CTG CGA GGC CCG GCC TCG GGG CCG GAG AGA GGC CAC CGG CAG ACC GTC CGC GTC CTG  
 S S R R P L R G P A A S G R E R G H R Q T V R V L

FIG. 6A

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(Donor A)  
CgtAAGTGGAGCCGCGTGGTTCCAAAGACGCCTGCCTGCAGTCCGCCCGCCGGGACCGCGCAACGCTGGGTCCCT  
TCCCCTGCTGCGCCAGCTCTGGGCGCGCTTCCAGCTCCCTTTCCTATTTCGATTCCAGCTCCACCGCCGgt...+569 bp  
(Donor B)

FM-1A: 7TM, 403 amino acids

IM6  
ag/CTG GTG GTG GTT CTG GCA TTT ATA ATT TGC TGG TTG CCC TTC CAC GTT GGC AGA ATC  
L V V V L A F I I C W L P F H V O R I  
IM7  
ATT TAC ATA AAC ACG GAA GAT TCG CGG ATG ATG TAC TTC TCT CAG TAC TTT AAC ATC GTC GCT CTG CAA CTT TTC  
I Y I N T E D S R M Y F S Q Y F N I V A L Q L F  
TAT CTG AGC GCA TCT ATC AAC CCA ATC CTC TAC AAC CTC ATT TCA AAG AAG TAC AGA GCG GCG GCC TTT AAA CTG  
Y L S A S I N P I L Y N L I S K K Y R A A A F K L  
CTG CTC GCA AGG AAG TCC AGG CCG AGA GGC TTC CAC AGA AGC AGG GAC ACT GCG GGG GAA GTT GCA GGG GAC ACT  
L L A R K S R P R G F H R S R D T A G E V A G D T  
GGA GGA GAC ACG GTG GGC TAC ACC GAG ACA AGC GCT AAC GTG AAG ACG ATG GGA TAA  
G G D T V G Y T E T S A N V K T M G \*

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FIG.6B

FM-1B: 5TM, 387 amino acids

CGT AAG TGG AGC CGC CGT GGT TCC AAA GAC GCC TGC CTG CAG TCC GCC CCG GGG ACC GCG CAA ACG CTG  
R K W S R R G S K D A C L Q S A P P G T A Q T L

GGT CCC CTT CCC CTG CTC GCC CAG CTC TGG GCG CCG CTT CCA GCT CCC TTT CCT ATT TCG ATT CCA GCC TCC ACC  
G P L P L L A Q L W A P L P A P F P I S I P A S T

CGC CGT GGT GGT TCT GGC ATT TAT AAT TTG CTG GTT GCC CTT CCA CGT TGG CAG AAT CAT TTA CAT AAA CAC  
R R G G S G I Y N L L L V A L P R W Q N H L H K H

GGA AGA TTC GCG GAT GAT GTA CTT CTC TCA GTA CTT TAA  
G R F A D D V L L S V L \*

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FIG.6C



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ATGCCCTGGACCAGACCCCAGGTGGACCTCCATGCTGCTGCAGCAGAGACCATGGACCAGTACACC  
ACGGACGACCACCACTACGAGGGCTCCCTCTTCCCCGCGTCCACCCTCATCCCCGTACGGTCATC  
TGCATCCTCATCTTCGTGGTCGGCGTGACCGGCAACACCATGACCATCCTCATCATCCAGTACTTC  
AAGGACATGAAGACCACCACCAACCTGTACCTGTCCAGCATGGCCGTGTCCGACCTCGTCATCTTC  
CTCTGCCTGCCCTTCGACCTGTACCGCCTGTGGAAGTACGTGCCGTGGCTGTTTCGGCGAGGCCGTG  
TGCCGCCTCTACCACTACATCTTCGAAGGCTGCACGTGCGCCACCATCCTCCACATCACGGCCCTG  
AGCATCGAGCGCTACCTGGCCATCAGTTCCCCCTCAGGAGCAAGGTGATGGTGACCAGGAGAAGG  
GTCCAGTACATCATCCTGGCCCTGTGGTGCTTCGCCCTGGTGTCGGCCGCTCCACGCTCTTCCTG  
GTCGGGGTGGAGTACGACAACGAGACGCACCCCGACTACAACACGGGCCAGTGCAAGCACACGGGC  
TACGCCATCAGCTCGGGGCAGCTGCACATCATGATCTGGGTGTCCACCACCTACTTCTTCTGCCCG  
ATGCTGTGTCTCCTCTTCCTCTACGGCTCCATCGGGTGCAAGCTGTGGAAGAGCAAGAACGACCTG  
CAGGGCCCGTGCGCCCTGGCCCGGAGAGGTGCGCACAGGCAAACGGTGAAGATCCTGGTGGTGGTG  
GTGCTGGCCTTCATCATCTGCTGGCTGCCCTACCACATCGGCAGGAACCTGTTGCCCAGGTGGAC  
GACTACGACACGGCCATGCTCAGCCAGAATTTCAACATGGCCTCCATGGTGCTCTGCTACCTCAGC  
GCCTCCATCAACCCCGTCGTCTACAACCTGATGTCGAGGAAGTACCGGGCCGCCGCAAGCGCCTC  
TTCCTGCTCCACCAGAGACCCAAGCCGGCCACCGGGGCGAGGGGCAGTTTTGCATGATCGGCCAC  
AGCCCCACCCTGGACGAGAGCCTGACGGGGGTGTGA

FIG.7

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MPWTRPQVDLHAAAAETMDQYTTDDHHYEGSLFPASTLIPVTVICILIF W GVTGNT  
MTILIIQYFKDMKTTTNLYLSSMAVSDLVIFLCLPFDLYRLWKYVPWLFGEAVCRLY  
HYIFEGCTSATILHITALSIERYLAISFPLRSKVMVTRRRVQYIILALWCFALVSAA  
PTLFLVGVEYDNETHPDYNTGQCKHTGYAISSGQLHIMIWVSTTYFFCPMLCLFLY  
GSIGCKLWKSKNLQGPCALARERSHRQTVKILVVVVLAFIICWLPHYHGRNLFAQV  
DDYDTAMLSQNFNMAVMVLCYLSASINPVVYNLMSRKYRAAAKRLFLLHQRPKPAHR  
GQGQFCMIGHSPTLDESLTGV

FIG.8

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pu75E7 1 ..MPWTRPQVDLHAAAAETMDQYTTDDHHYEGSLFPASTLIPVTVICILI 48
      ||      |      ||      ||      ||      ||      ||      ||
huMTLR 1 MGSPWNGS..DGPEGAREPPWPALPPCDERRCSPFPLGALVPVTAVCLCL 48

      49 FVVGVTGNTMTILIIQYFKDMKTTTNLYLSSMAVSDLVIFLCPLPFDLYRL 98
      |||||.||.:::|::|:||||| |||||. | |||||
      49 FVVGVSQNVVTVMILIGRYDMRTTTNLYLGSMASDLLILLGLPFDLYRL 98

      99 WKYVPWLFGEAVCRLYHYIFEGCTSATILHITALSIERYLAISFPLRSKV 148
      |: ||.||. ||| |: |||| ||: ||. ||||: ||||| |||.:|
      99 WRSRPWFVGPLLCRLSLYVGEGCTYATLLHMTALSVERYLAICRPLRARV 148

      149 MVTRRRVQYIILALWCFALVSAAPTFLVGV EYD..... 182
      :|||||. :| || ||. || | ||||| |
      149 LVTRRRVRALIAVLWAVALLSAGPFLFLVGV EQDPGISVVPGLNGTARIA 198

      183 .....NETHPDYNTGQCKHTGYAISS.....GQLHIM 209
      | .| .| :| | :|
      199 SSPLASSPPLWLSRAPPSPSPSGPETAEAAALFSRECRPSPAQLGALRVM 248

      210 IWVSTTYFFCPMLCLLFLYGSIGCKLWKSNDLQGPCALARERSHRQTVK 259
      :|||. | || | || | || | || | :| |. || | || | ||||:
      249 LWVTTAYFFLPFLCLSILYGLIGRELWSSRRPLRGPAASGRERGHRTVR 298

      260 ILVVVVLAFIICWLPYHIGRNLFAQVDDYDTAMLSQNFNMASMLCYLSA 309
      :|. ||||| |||||:|: || :| :| ||. :| ||||
      299 VLLVVVLAFIICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQLFYLSA 348

      310 SINPVVYNIMSRRYRAAAKRLFLLHQ.RPKPAHRGQ...GQFCMIGHSP 355
      ||||:|. |||. |: ||||| :| | . ||: || . | :|
      349 SINPILYNLISKKYRAAAFKLLARKSRPRGFHRSRDTAGEVAGDTGGDT 398

      356 LDESLTGV..... 363
      . . |
      399 VGYTETSANVKTMG 412

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FIG.9

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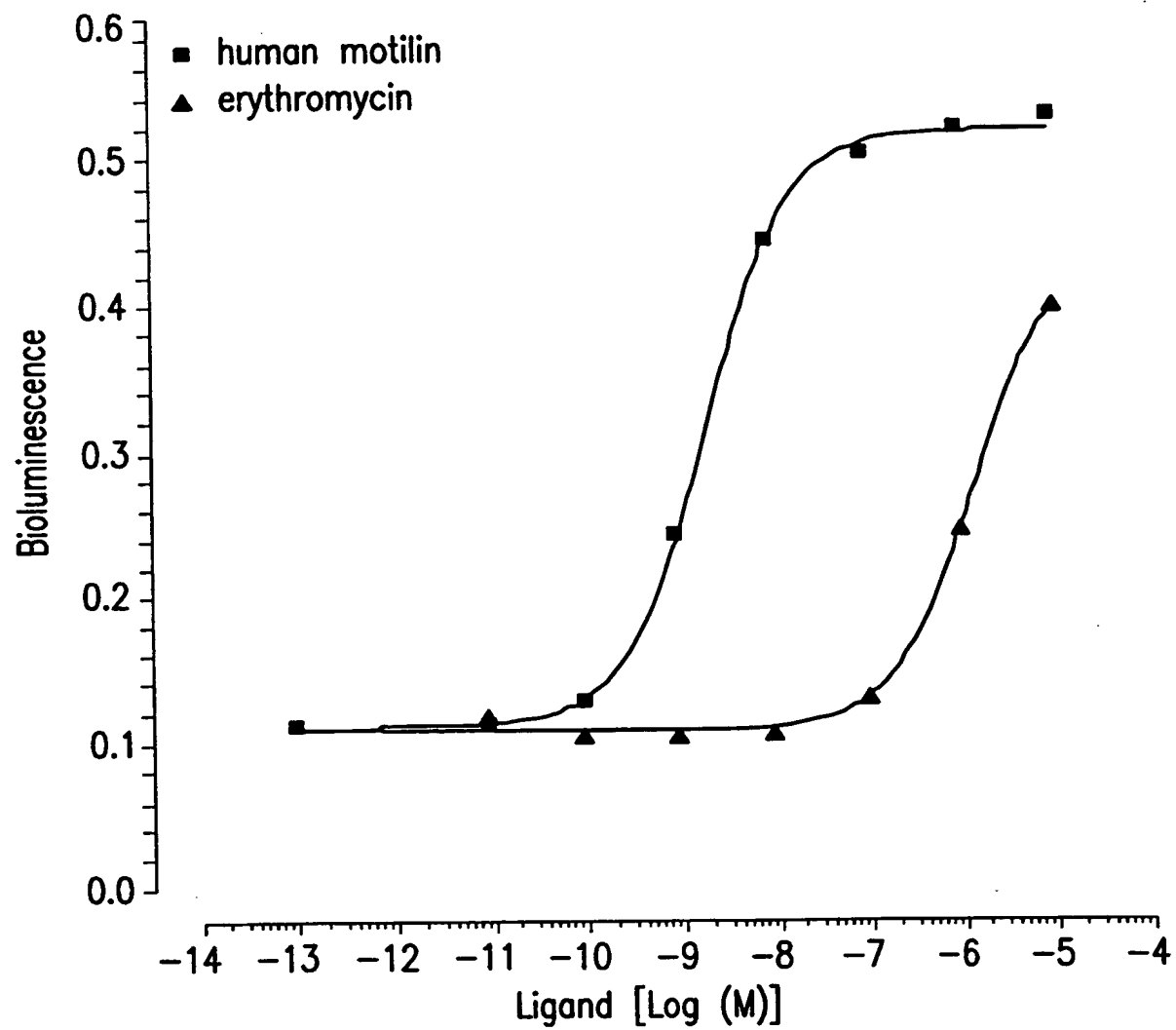


FIG.10

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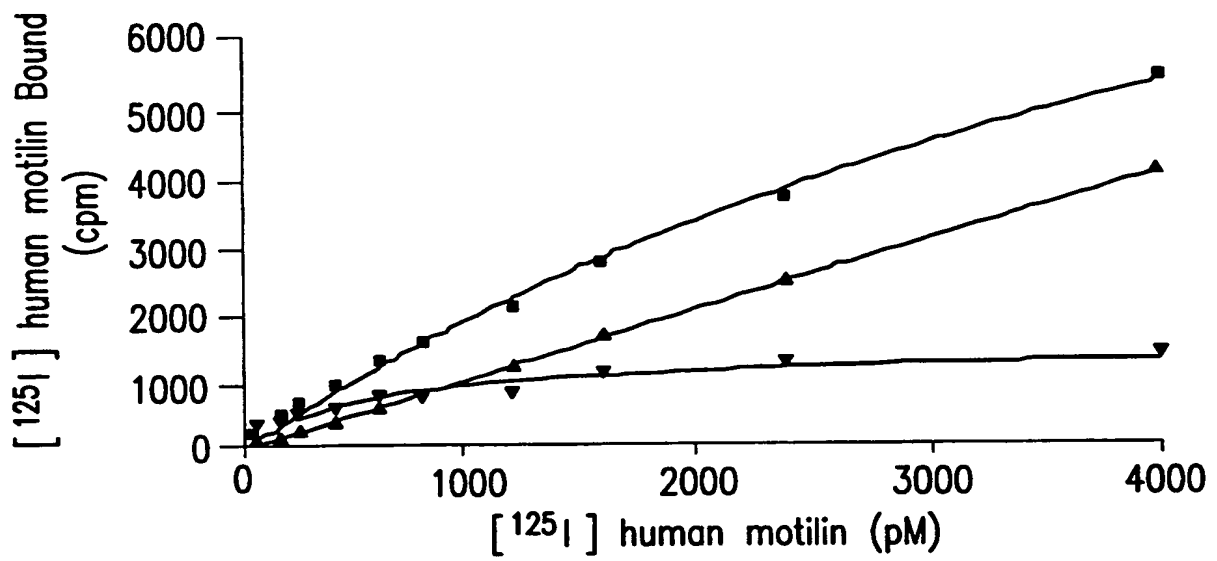


FIG. 11